Docket No.: 4661-0113PUS1 App No.: NEW

Inventor: Sarman SINGH et al.

Title: POLYPEPTIDES FOR THE DIAGNOSIS AND THERAPY

OF LEISHAMANIASIS

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Figure 1

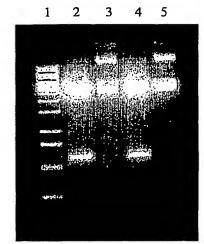
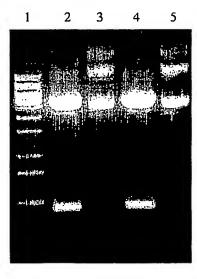


Figure 2



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Figure 3A

Query:	40	EGRAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXIAEVRAAELAGVLEATAAAKTAV	99

E RAAELA +LEATA+AK+ EQD +E RAAELA LEATAAAK +

Sbjct: 712 EERAAELASQLEATAAAKSSAEQDRENTRATLEQQLRESEARAAELASQLEATAAAKMSA 771

EQ+RE TRA L K S EQ

Sbjct: 772 EQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEER 831

Query: 160 XXXXXXXXXXSTAAVKSAMEQDRENTRAT 187

+ST A K + EQDRE+TRAT

Sbjct: 832 AAELASQLESTTAAKMSAEQDRESTRAT 859

Figure 3B

- Query: 29 EQEREKTRTALE------GRAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXXXIAEVR 81
 - EQ+RE TR LE RAAELA +LEATA+AK EQD +E R
- Sbjct: 733 EQDRENTRATLEQQLRESEARAAELASQLEATAAAKMSAEQDRENTRATLEQQLRDSEER 792

AAELA LE+T AAK + EQ+RE TRA L K S EQ

Sbjct: 793 AAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQD 852

+ST A K + EQDRE+TRAT

Sbjct: 853 RESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQDRESTRAT 898

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Figure 3C

Query: 29	EQEREKTRTAL	LEGRAAELA	RAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXIAEVR				
	EQ+RE TR I	LE RAAELA	+LE+T +AK	EQD	+E R		

Sbjct: 772 EQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEER 831

Sbjct: 832 AAELASQLESTTAAKMSAEQDRESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQD 891

++TAA KS+ EQDRENTRA

Sbjct: 892 RESTRATLEQQLRDSEERAAELASQLEATAAAKSSAEQDRENTRA 936

Figure 3D

Query: 40 EGRAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXIAEVRAAELAGVLEATAAAKTAV 99

E RAAELA +LEATA+AK+ EQD +E RAAELA LEATAAAK +

Sbjct: 712 EERAAELASQLEATAAAKSSAEQDRENTRATLEQQLRESEARAAELASQLEATAAAKMSA 771

EQ+RE TRA L K S EQ

Sbjct: 772 EQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEER 831

Query: 160 XXXXXXXXXXXXAAVKSAMEQDRENTRAT 187

+ST A K + EQDRE+TRAT

Sbjct: 832 AAELASQLESTTAAKMSAEQDRESTRAT 859

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Figure 3E

Query: 29	EQEREKTRTALEGRAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXXIAEVR 81						
	EQ+RE TR	ΓE	RAAELA +LE	EATA+AK	EQD	+E R	

Sbjct: 733 EQDRENTRATLEQQLRESEARAAELASQLEATAAAKMSAEQDRENTRATLEQQLRDSEER 792

Sbjct: 793 AAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQD 852

+ST A K + EQDRE+TRAT

Sbjct: 853 RESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQDRESTRAT 898

Figure 3F

- Query: 29 EQEREKTRTALEG-----RAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXXXIAEVR 81
 EQ+RE TR LE RAAELA +LE+T +AK EQD . +E R
- Sbjct: 772 EQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEER 831
- Sbjct: 832 AAELASQLESTTAAKMSAEQDRESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQD 891

++TAA KS+ EQDRENTRA

Sbjct: 892 RESTRATLEQQLRDSEERAAELASQLEATAAAKSSAEQDRENTRA 936

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Figure 4

LCIMM	121	GAGCAGCAGCTTCGCGAATCCGAGGCGCGCGCGCGCGCGAGCCAGCTGGAGGCC	180
KEIMM	1		1
DDIMM	1	GAGCAGCAGCTTCGTGAATCCGAGGCGCGCGCGCGGAGCTGAAAGCCGAGCTGGAGGCC	_
LCIMM	181	ACTGCTGCTGCGAAGATGTCAGCGGGGGCAGGGGCCACGCTAGAG	240
KEIMM	1		3
DDIMM	61	ACTGCTGCTGCGAAGACGTCGGTGGAGCAGCGTGAGAAGACGAG	107
DDIMM	241	CAGCAGCTTCGTGACTCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGTCCACT	300
KEIMM	4	CAGCAGCTTCGTGACTCCGAGGAGCGCGCTGCGGAGCTGATGCCGAAGTTAGAGGCGACT	63
FGIMM	108	GA-CGGCTCTGGAGGGGCGCGCTGCGGAGCTGGCTCCCAAACTGGAGGCGACT	159
LCIMM	301	ACTCCTGCGAAGATGTCACCGGAGCAGGACCGCGAGAGCACGACGACGACACGCTAGAGCAG	360
REIMM	64	CCTCCTGCGAAGTCGTCGCGGGAGCAGGACCGCGAGAACACGAGGGCCACGTTGGAGCAG	123
DDIMM	160	CCTTCTGCGAAGAATTTGGTAGAGCAGGACCGCGAGAGGACGAGGGCCACCTTGGAGGAA	219
LCIMM	361	CAGCTTCGTGACTCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGTCCACTACT	420
KEIMM	124	CAGCTTCGCGAATCCGAGGAGCACGCTGCGGAGCTGAAGGCCCAGCTGGAGTCCACTGCT	183
DDIMM	220	CGACTTCGTATTGCTGAGGTGCGCGCGCGGAGCTGCAGGAGTGCTGGAGGCCACTGCT	279
LCIMM	421	GCTGCGAAGATGTCAGCGGAGCAGGACCGGGAGAGCACGAGGGCCACGCTAGAGCAGCAG	480
KEIMM	184	GCTGCGAAGACGTCGGCGGAGCAGGACCGCGAGAACACGAGGGCCGCGTTGGAGCAGCG	243
DDIMM	280	GCTGCGAAGACGGCGGTGGAGCAGGAGGACGAGGGCCGCCTTGGAGCAGCAG	339
LCIMM	481	CTTCGCGAATCCGAGCAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGTCCACTACTGCT	540
KEIMM	244	CTTCGCGAATCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGGCCACTGCTGCT	303
DDIMM	340	CTCCGCGAATCCGAGGCGCGCGCTGCGGAGCTGGCTGCGCAGCTGGAAGCCGCTGCTGCG	399
LCIMM	541	GCGAAGATGTCAGCGGAGCAGGACCGCGAGAGCACGAGGGCCACGCLAGAGCAGCATT	600
KRIMM	304	GCGAAGTCGTCGGCGGAGACCGCGAGAACACGAGGGCCACGCTAGAGCAGCAGCTT	363
DDIMM	400	GCGAAGACGTCGGTGGAGCAGCAGCGTGAGAACACGAGGGCCACCTTGGAGGAGCGGTTG	459
LCIMM	601	CETGACTCCGAGGAGCGCCTGCGGAGCTGGCGAGCCAGCTGGAGGCCACTGCTGCTGCG	660
KEIMM	364	CGCGAATCCGAGGCGCGCGCTGCGGAGCTGGGAGTCAGCTGCAGCTGCTGCTGCTG	423
DDIMM	460	CGGCTCGCTGAGGTCCGCGCTGCGGAGCTGGCAGCGGCTAAAGAGCACCTGCTGCTGTT	519
LCIMM KEIMM DDIMM	661 424 520	AAGTCGTCGCGGGAGCAGGACCGCGAGAACACGAGGGCCGCTTGGAGCAGCAGCTTCGT AAGTCGTCGGCGGAGCAGGACCGCGAGAACACGAGGGCCACGAAGTCCGCGATGGAGCAGGACCGCGAGAACACGAGGGCCACG	720 465 561

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Figure 5

LCIMM	1	leqqlreseeraaelasqleataaakssaeqdrentratleqqlresearaaelasqleä	60
KEIMM	1	-eqqlrdseeraaelmrkleataaakssaeqdrentratleqqlreseehaaelkaqles	59
DDIMM	1	-eqqlrëse <mark>araaelkaëleataaak</mark> ësveqërektrtalegraaelarëleë	52
LCIMM	61	TAÄAKMSAEQDRENTRALLEÕOLRDSEERAAELASQLESTTAAKMSAEQÖRESTRATLEQ	120
KEIMM	60	TAAAKTSAEQDRENTRAALEQRLRESEERAAELASQLEATAAAKSSAEQDRENTRATLEQ	119
DDIMM	53	TAŚAKNIVEODRERTRATLEĘRLRIĄEVRAAELAGVLEĄTĄAAKTĄVEOĘRERTRAĄLEO	112
LCIMM	121	QLRÖSE <mark>ERAAELASQLESTTAAKMSAEQÖRESTRAT</mark> LEQQLRESEERAAELASQLESTTA	180
KEIMM	120	QLRESEARAAELASQLESTAAAKSSAEQDRUNTRAT	155
DDIMM	113	QLRESEARAAELAAOLENAAAKTSVEQERENTRATLEERLRLAEVRAAELAARLKSTAA	172
LCIMM	181	AKMSAEQDRESTRATLEQQLRDSEERAAELASQLEATAAAKSSAEQDRENTRAALEQQLR	240
KEIMM	155		155
DDIMM	173	VKSAMEQDRENTRAT	187
		Figure 6	
LCIMM	. 1	LEQQLRESEERAAELASQLEATAAAKSSAEQDRENTRATL <mark>EQQLRESEARAAEL</mark> A <u>SQ</u> LEA	60
DDIMM	1	EQQLRESEARAAEL KAE LEA	20
LCIMM	61	TAAAKMSAEQDRENTRATLEQQLRDSEERAAELASÕLESTTÄAKMSAEQDRESTRATLEÕ	120
DDIMM	21	TAAAKTSVEOËREKTRTALEGRAAELARKLEÄTASAKNLVEODRERTRATLEË	73
LCIMM	121	<u>ÖLRDSEBRAAELASQLESTTAAKMSAEQDRESTRATLEQQLRESEBRAAELASQLESTTA</u>	180
DDIMM	74	rlriāevraaelagvleātaaaktāveqërertraaleqolresearaaelaāqle <u>ā</u> aaa	133
LCIMM	181	AKMSAEQDRESTRATLEOOLRDSEERAAELASOLEATAAAKSSAEQDRENTRAALEQQLR	
DDIMM	134	AKTSVEOERENTRATLEERLRLÆEVRAAELAARLKSTAAVKSAMEQDRENTRAT	187

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Figure 7

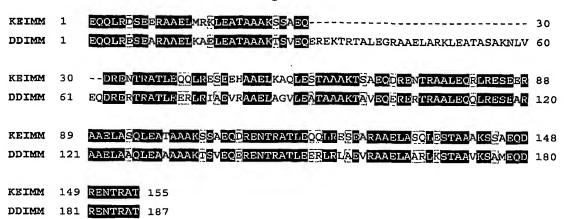


Figure 8

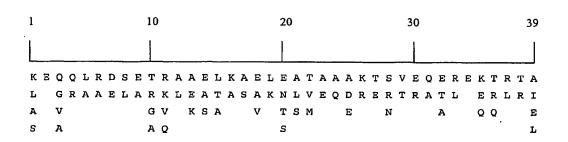
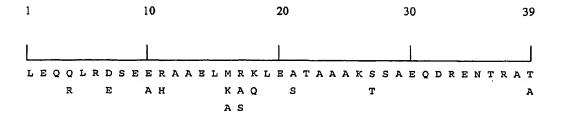


Figure 9



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Figure 10

b) a)

Figure 11

a) b)





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Figure 12

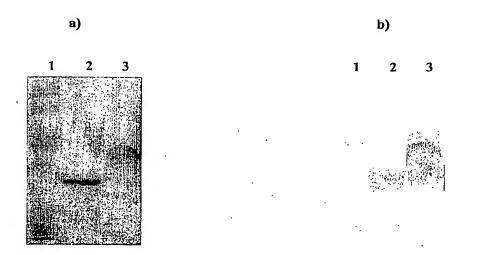
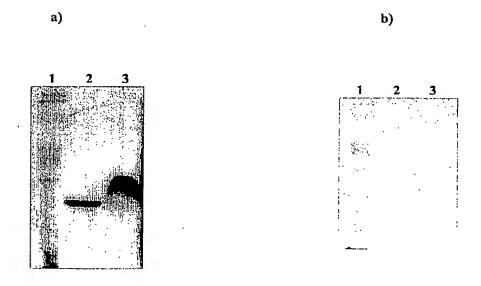


Figure 13



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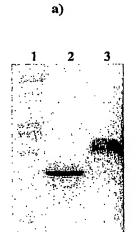
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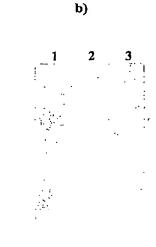
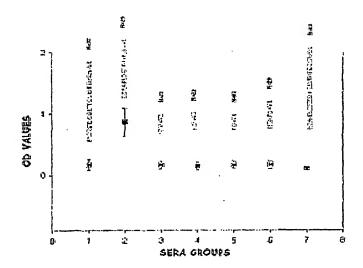


Figure 15



Mean!	0.1670	0.8665)	0.1634	0.1396	0.1663	0.1636]	0.1080
Std.Dev		0.2182	0.0598	0.0584	0.0534	0.0615	0.0295

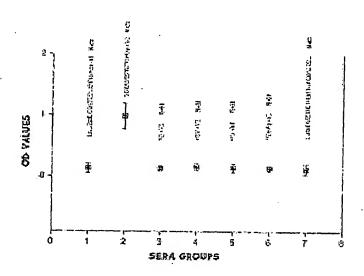
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Figure 16



Mean	0.1290	0.9730	0.1300)	0.15451	0.14561	0.13631	0.12191
Std Dev	0.0716	0.2096	0.0419	0.0548	0.0705	0.0456	0.0796